

MS-Fit Search Results

[-] Parameters

Database searched: **User Protein**Digest Used: **Trypsin**Max. # Missed Cleavages: **1**Constant Modification: **Propionamide (C)**Sample ID (comment): **20170104TKS_No2_sample2(NC1-)**Minimum Matches: **1**Sort Type: **Score Sort**Considered modifications: | **Peptide N-terminal Gln to pyroGlu** | **Oxidation of M** | **Protein N-terminus Acetylated** |Min Parent Ion Matches: **1**MOWSE On: **1**MOWSE P Factor: **0.4**Report Homologous Proteins: **Interesting**

[+] Pre Search Results (User Protein)

Fraction-Spot-Run ID: **1-1-1**MS-Fit search selects **1** entry.

[-] Results Summary

| Protein Hit Number | MOWSE Score | # pep # mat % mat | % Cov | % TIC | Mean Err Da | Data Tol Da | # Hom Prot | MS-Digest Index # | Protein MW (Da)/pI | Accession # | Species | Protein Name |
|--------------------|-------------|-------------------|-------|-------|-------------|-------------|------------|-------------------|--------------------|-------------|------------|--------------|
| 1 | 661 | 6/5/71 | 4.6 | 71.4 | 0.0506 | 0.204 | No | 1 | 175661/4.2 | 1 | UNREADABLE | |

[-] Detailed Results

1. 5/7 matches (71%).

Acc. #: 1 Species: UNREADABLE Name:

Index: 1 MW: 175661 Da pI: 4.2

| m/z Submitted | MH ⁺ Matched | Intensity | Delta Da | Modifications | Start | End | Missed Cleavages | Sequence |
|---------------|-------------------------|-----------|----------|----------------|-------|------|------------------|--------------------------|
| 996.4185 | 996.4421 | 100.0 | -0.0236 | 1Gln->pyro-Glu | 1417 | 1424 | 0 | (K)QNQDFFSK(V) |
| 996.4185 | 996.5360 | 100.0 | -0.118 | | 1167 | 1174 | 0 | (K)LEEVHELK(E) |
| 1277.6764 | 1277.6107 | 100.0 | 0.0657 | | 1155 | 1165 | 0 | (K)EVSSLEVVEEK(K) |
| 1582.8488 | 1582.7456 | 100.0 | 0.103 | | 214 | 226 | 0 | (K)SVQQEQQHNVEEK(V) |
| 1618.8612 | 1618.7330 | 100.0 | 0.128 | | 1189 | 1202 | 0 | (K)GLEEDDLEEVDDLK(G) |
| 2045.1761 | 2045.0285 | 100.0 | 0.148 | | 891 | 908 | 1 | (K)SESDVITVEEIKDEPVQK(E) |

Num Unmatched Masses: **2**

Search for disulfide linked peptides.

Do a non-specific cleavage search.

Search for another component.

The matched peptides cover **4.6%** (72/1558AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 1

The matched peptides cover 4.6% (72/1558AA's) of the protein.

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1  MTNSNYKSNM KTYNENNEQ ITTIFNRTNM NPIKKCHMRE KINKYFFLIK ILTCTILIWA VQYANNSDIN KSWKNTYVD
81  KKLNLKLFNRS LGESQVNGEL ASEEVKEKIL DLLEEGNTLT ESVDNKNLE EAEDIKENIL LSNIIEPKEN IIDNLLNIG
161 QNSEKQESVS ENVQVSEDLF NELLNSVDVN GEVKENILEE SQVNDIFNS LVKSVQQEQQ HNVEEKVEES VEENDEESVE
241 ENVEENVEEN DDESVAASSVE ESIASSVDES IDSSIEENVA PTVEEIVAPT VEEIVAPSVV ESVAPSVEES VEENVEESVA
321 ENVEESVAEN VEESVAENVE ESAENVEES VAENVEESVA ENVEEIVAPT VEESVAPTVE EIVAPSVEES VAPSVEEIVV
401 PTVEESVAEN VEEIVAPSVE EIVAPSVEEI VAPTVEESVA PTVEEIVAPS VEESVAPSVE EIVVPTVEES VAENVEESVA
481 ENVEEIVAPS VEEIVAPSVE EIVAPSVEEI VAPSVEEIVA PSVEEIVAPS VEEIVAPSVE EIVAPSVEEI VAPTVEEIVA
561 PTVEEIVAPS VEEIVAPTVE ESAENVATN LSDNLLSNLL GGIETEEIKD SILNEIEEVK ENVVTTILEN VEETTAESVT
641 TFSNILEEIQ ENTITNDTIE EKLEELHENV LSAALNTQS EEEKKEVIDV IEEVKEEVAT TLIETVEQAE EESASTITEI
721 FENLEENAVE SNENVAENLE KLNQTVFNTV LDKVEETVEI SGESLENNEM DKAFFSEIFD NVKGIQENLL TGMFRSIETS
801 IVIQSEEKVD LNENVVSSIL DNIENMKEGL LNKLENISST EGVQETVTEH VEQNVYVDVD VPAMKDQFLG ILNEAGGLKE
881 MFFNLEDVFK SESDVITVEE IKDEPVQKEV EKETVSIIEE MEENIVDVLE EEKEDLTDKM IDAVEESIEI SSDSKEETES
961 IKDKEKDVSL VVEEVQDNM DESVEKVLLEL KNMEEELMKD AVEINDITSK LIEETQELNE VEADLIKDME KLKELEKALS
1041 EDSKEIIDAK DDTLEKVIIE EHDITTTLDE VVELKDVEED KIEKVSDLKD LEEDILKEVK EIKELESEIL EDYKELKTIE
1121 TDILEEKKEI EKDHFEKFEE EAEEIKDLEA DILKEVSSLE VEEEKLEEV HELKEEVEHI ISGDAHIKGL EEDDLEEVD
1201 LKGSILDMLK GDMELGDMDK ESLEDVTAKL GERVESLKDV LSSALGMDEE QMKTRKKAQR PKLEEVLLEK EVKEEPKKKI
1281 TKKKVRFDIK DKEPKDEIVE VEMKDEDIDE DIEEDVEEDI EEDKVEDIDE DIDEDIDEDI GEDKDEVIDL IVQKEKRIEK
1361 VKEKKKLEK KVEEGVSLK KHVDEVMKYV QKIDKEVDKE VSKALESKND VTNVLKQNGD FFSKVKNFVK KYKVFAAPFI
1441 SAAAFASYV VGFFTFSLFS SCVTIASSTY LLSKVDKTIN KNKERPFYSF VFDIFKNLKH YLQMQKEKFS KEKNNNVIEV
1521 TNKAEKGNV QVTNKTEKTT KVDKNNKVPK KSRTQKSK

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[No2] sample2(NC1-)

